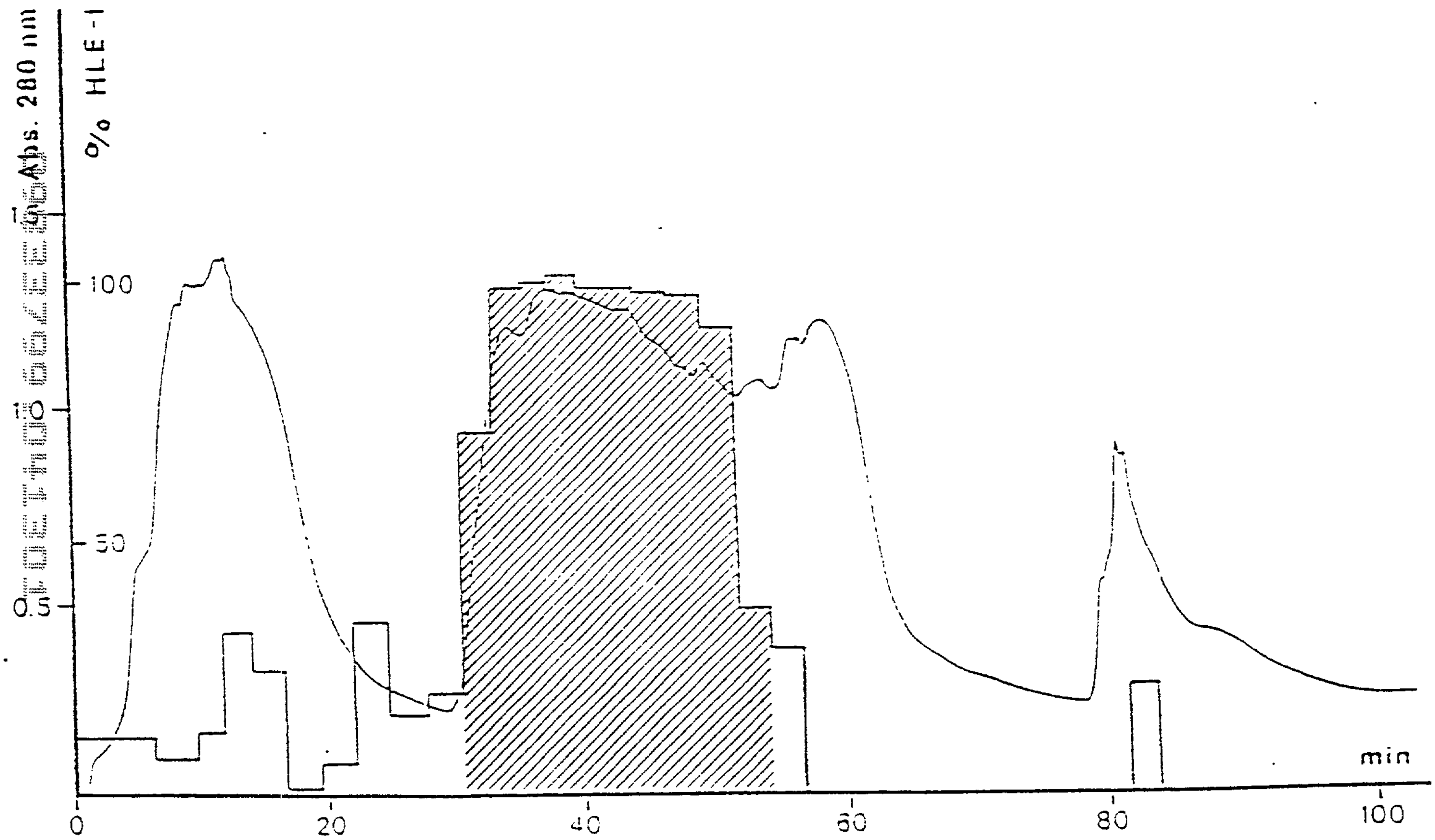


Fig. 1

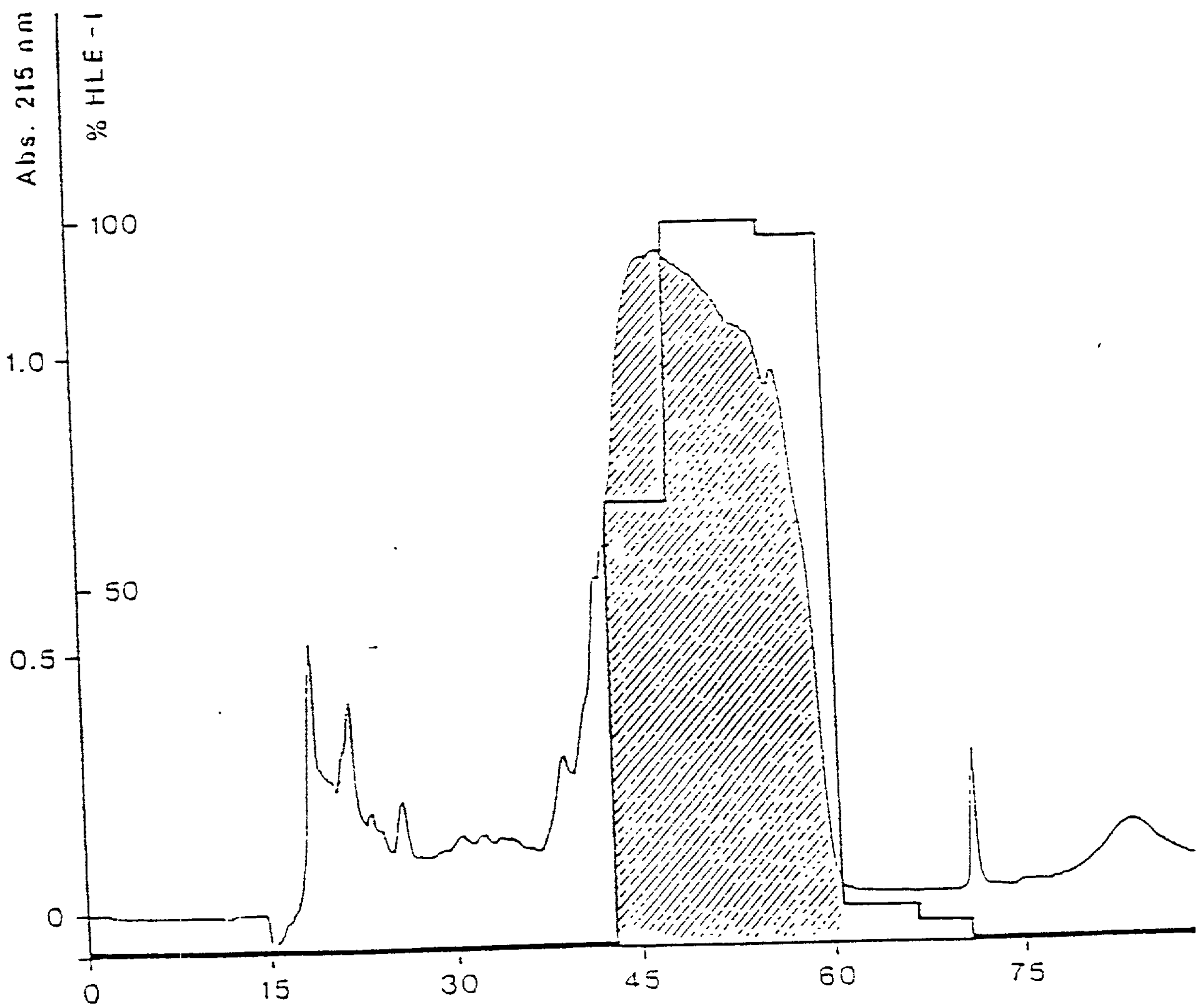


Fig. 2

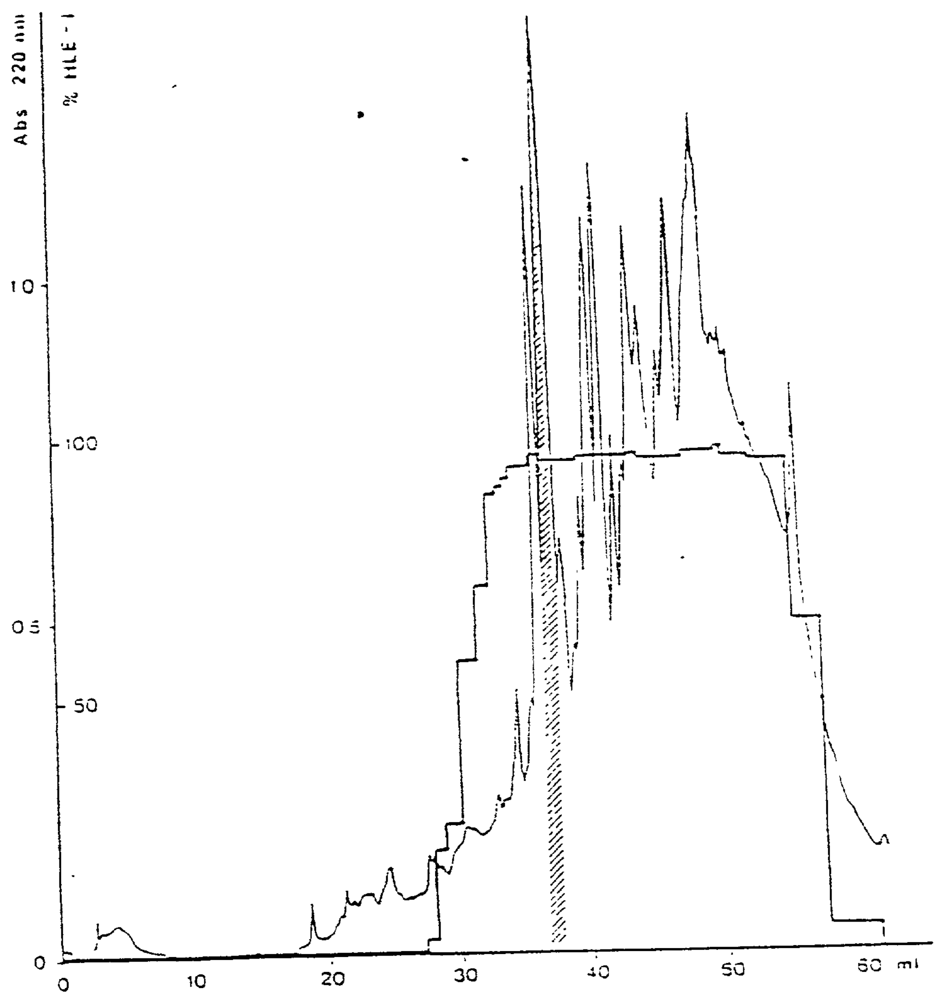


Fig. 3

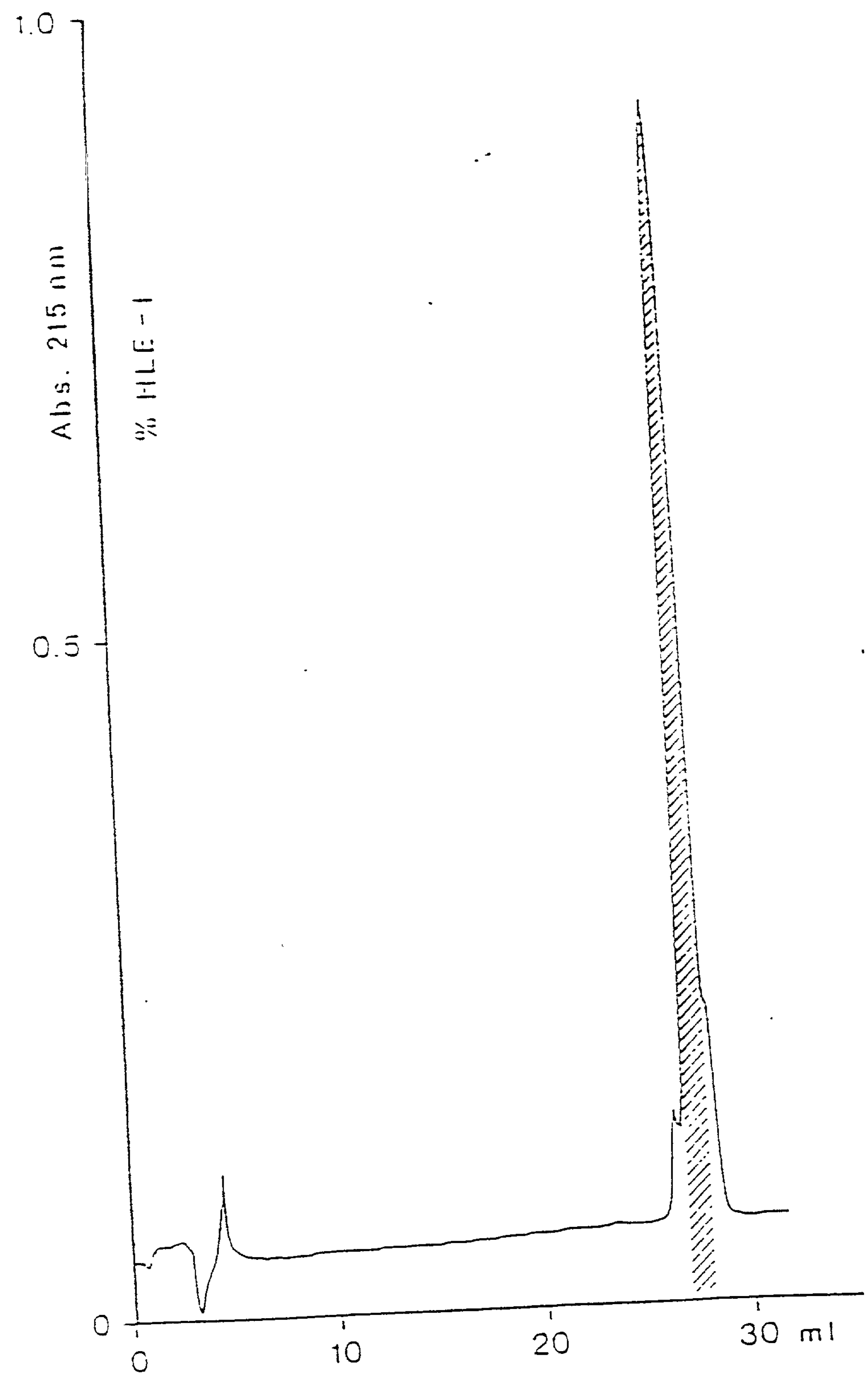


Fig. 4

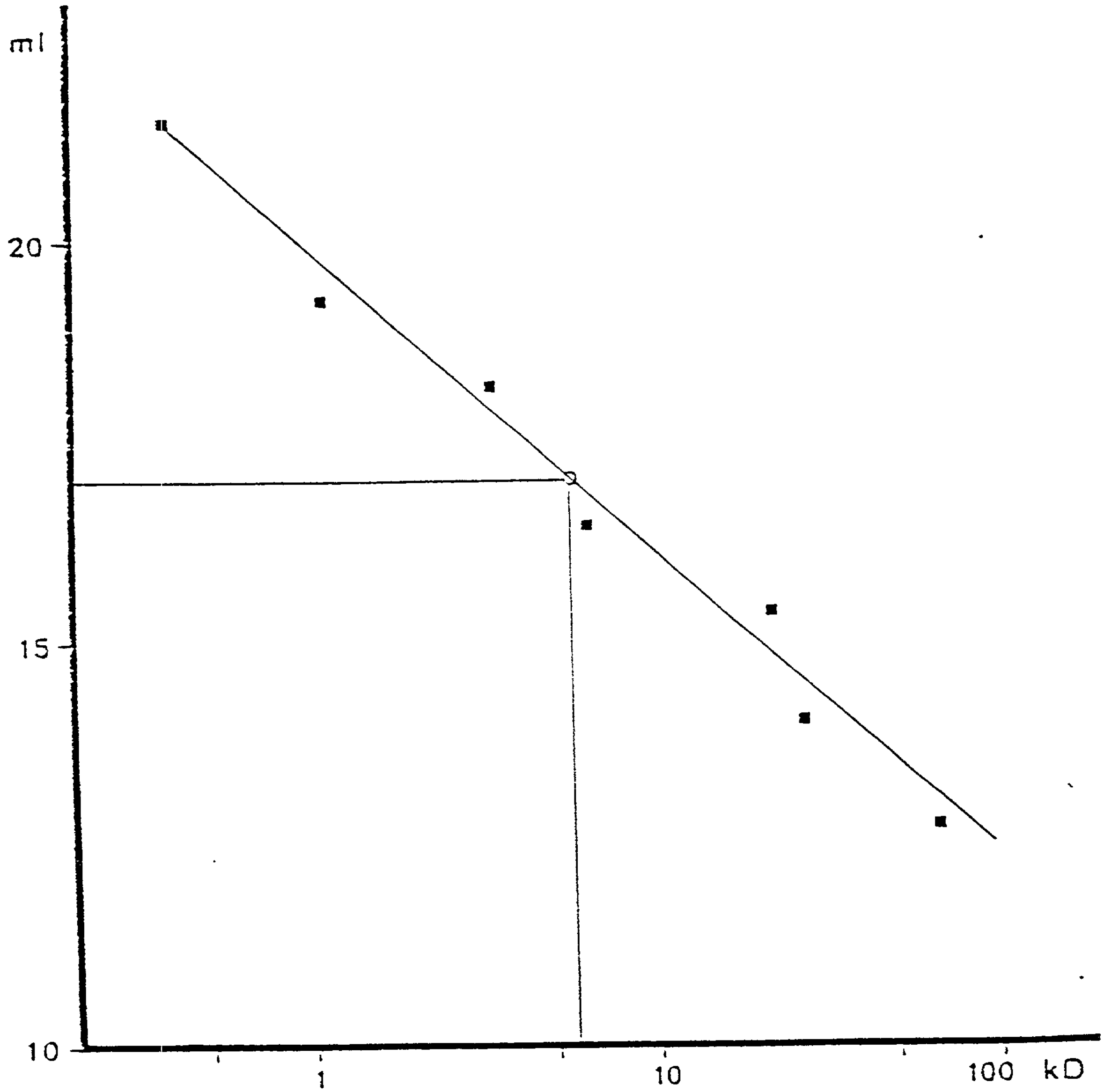


Fig. 5

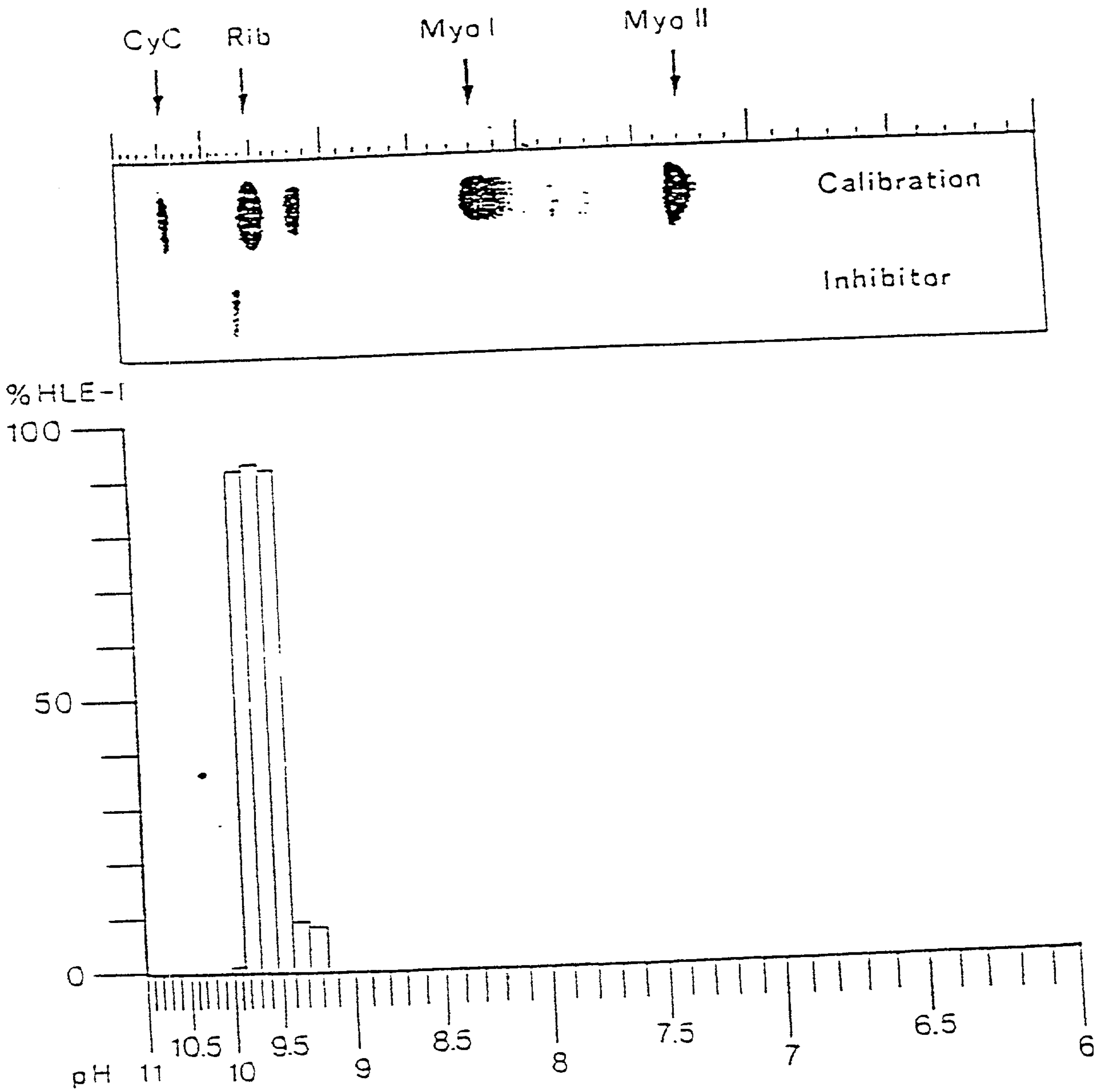

CyC
Rib
Myo I
Myo II
Calibration
Inhibitor
%HLE-I
100
50
0
pH
11
10.5
10
9.5
9
8.5
8
7.5
7
6.5
6

Fig. 6

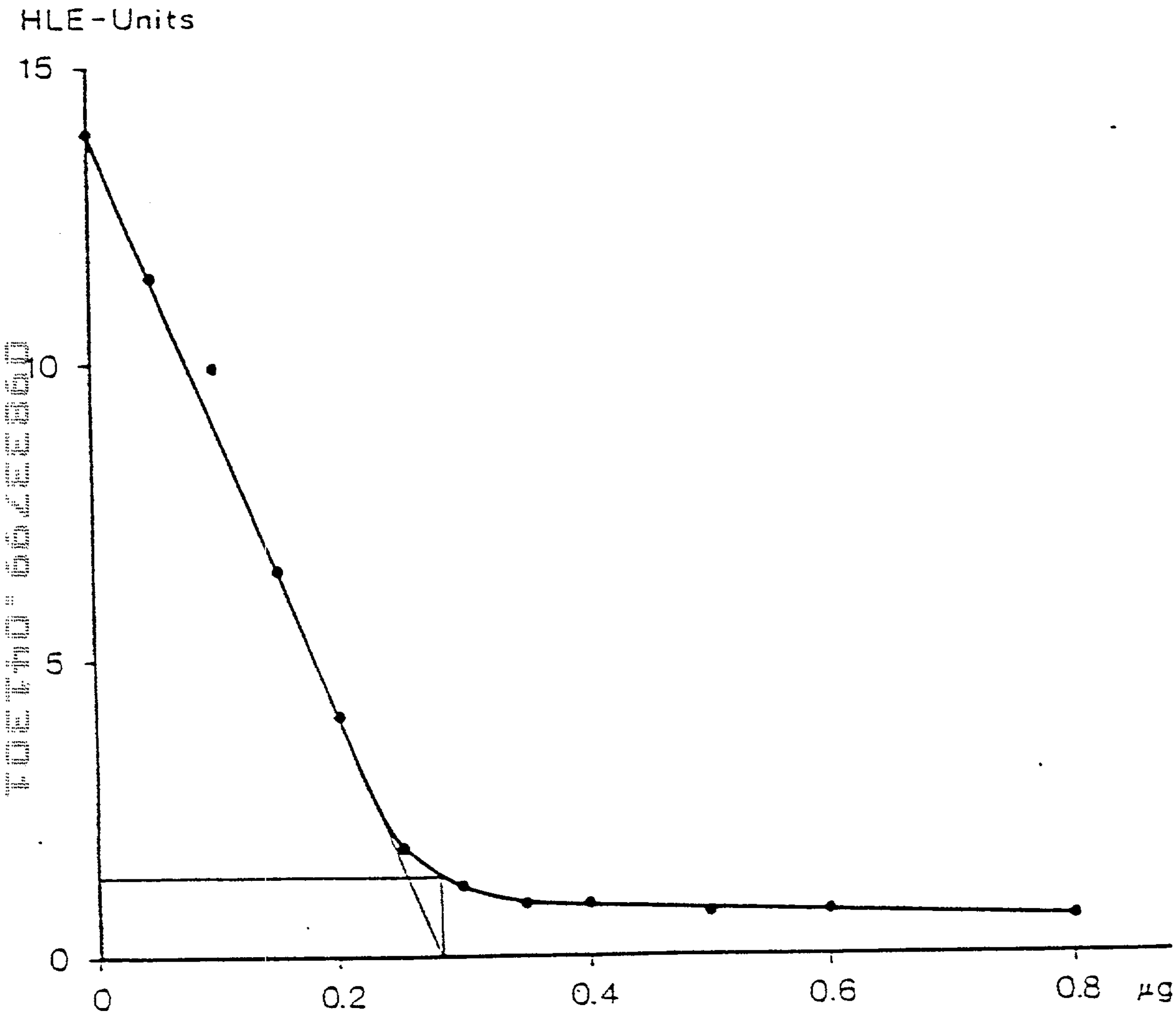
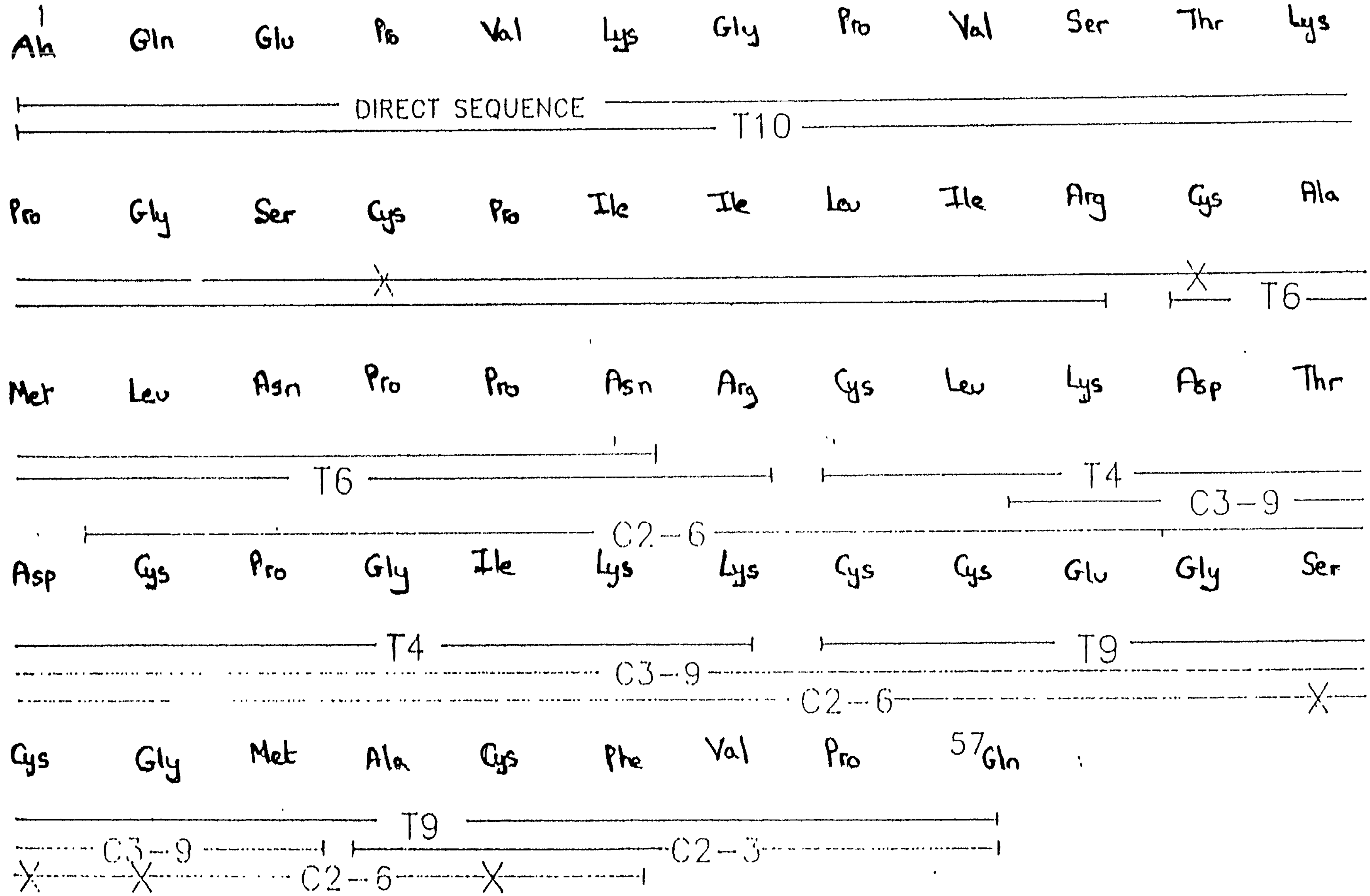


Fig. 7

FIGURE 8

PROTEIN SEQUENCE OF ELASTASE INHIBITOR



X=UNIDENTIFIED T=TRYPTIC FRAGMENTS C=CHYMOTRYPTIC FRAGMENTS

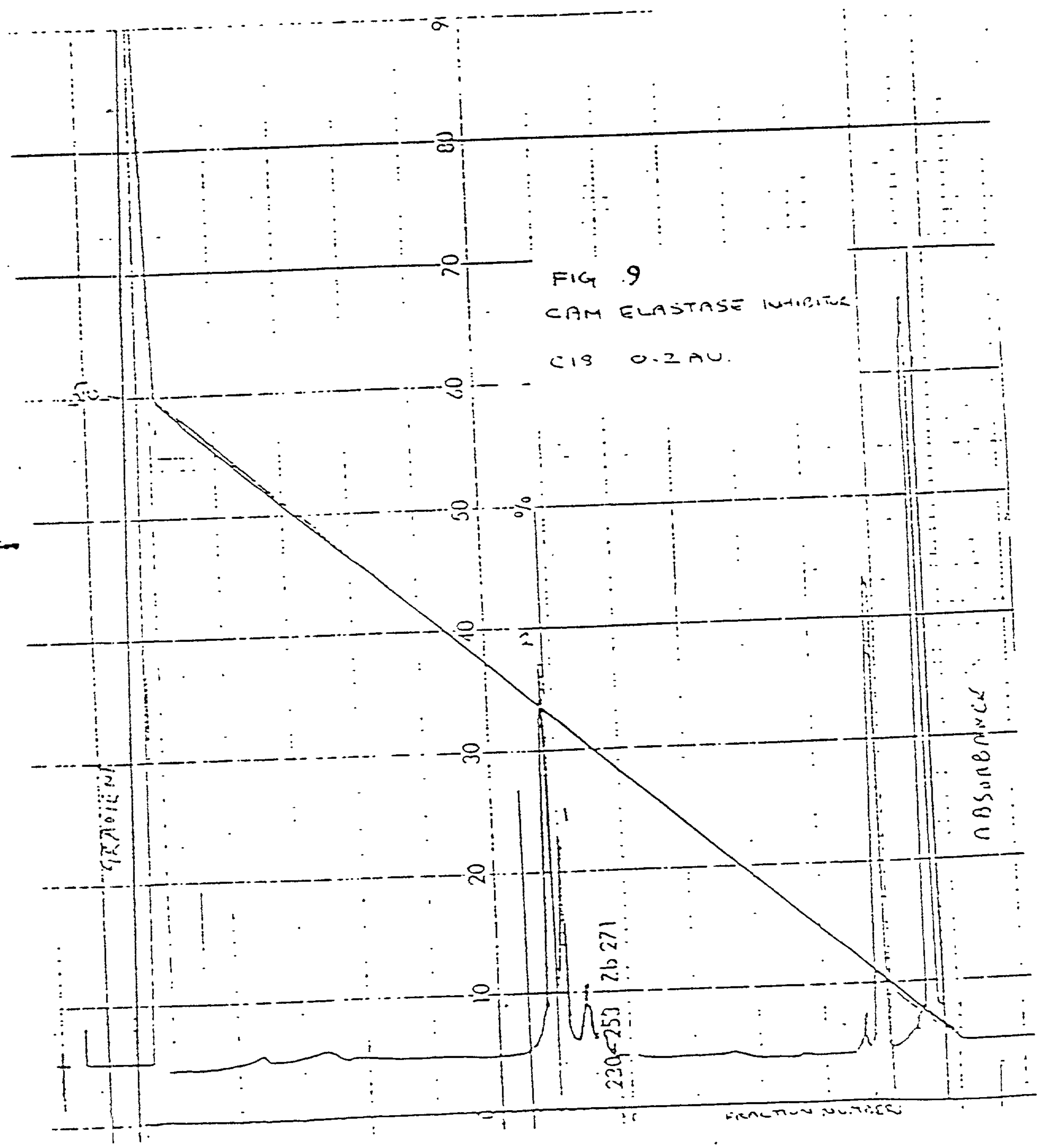


FIG 9
CAM ELASTASE INHIBITOR
C18 0.2AU
%
10
20
30
40
50
60
70
80
90
GRADIENT
ABSORBANCE
26 271
230-253
FRACTION NUMBER

FIG 9

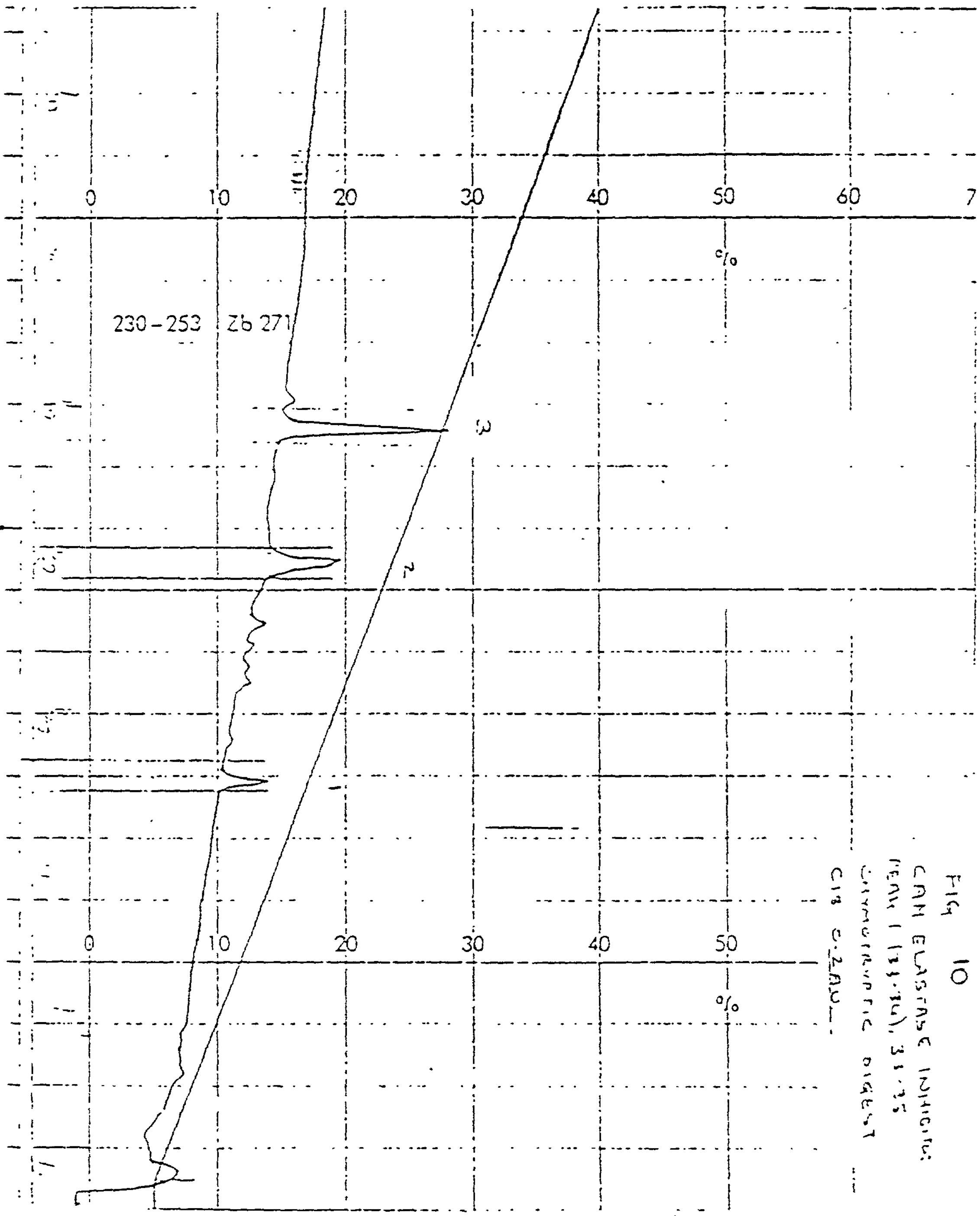


FIG 10

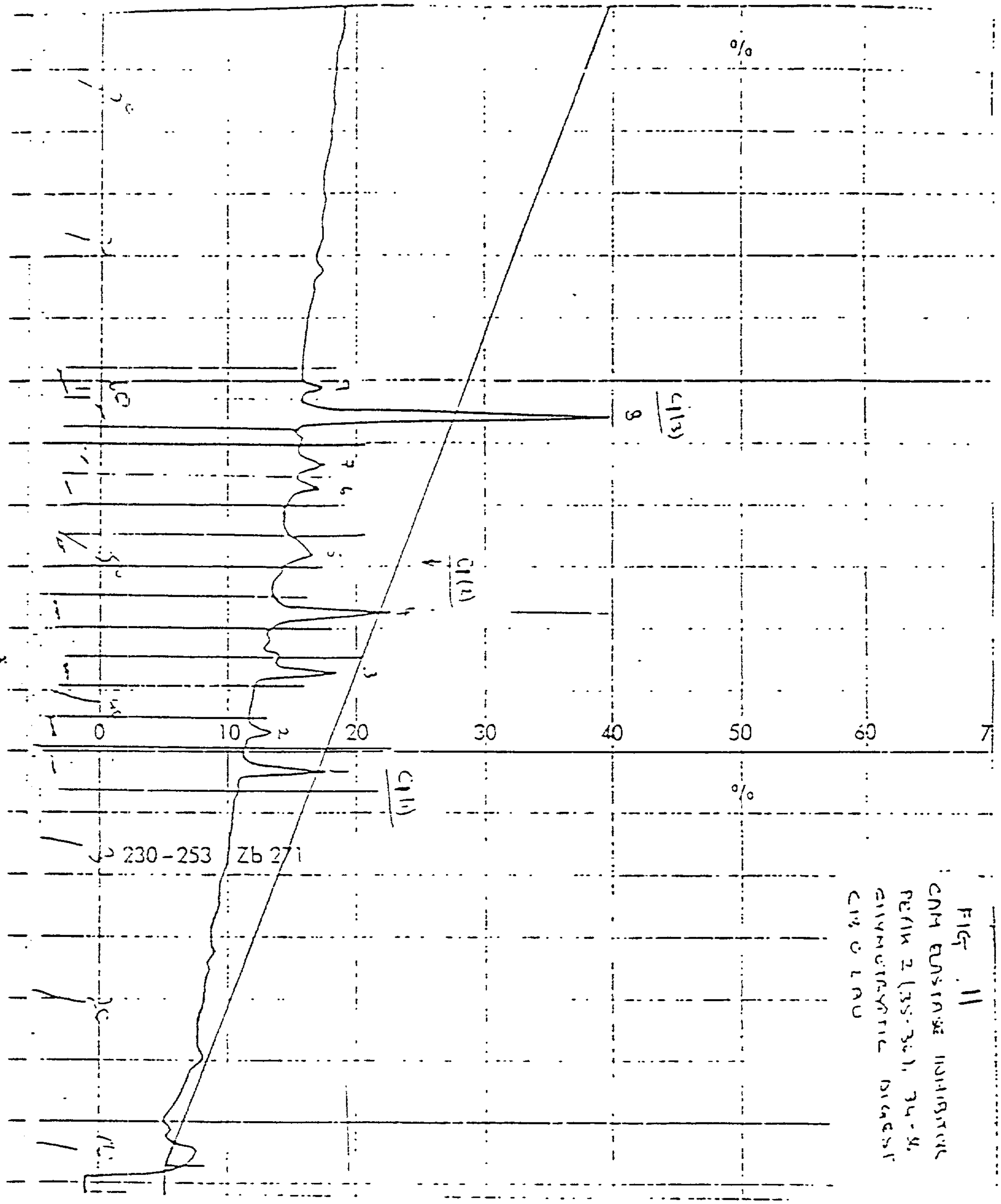


FIG 11

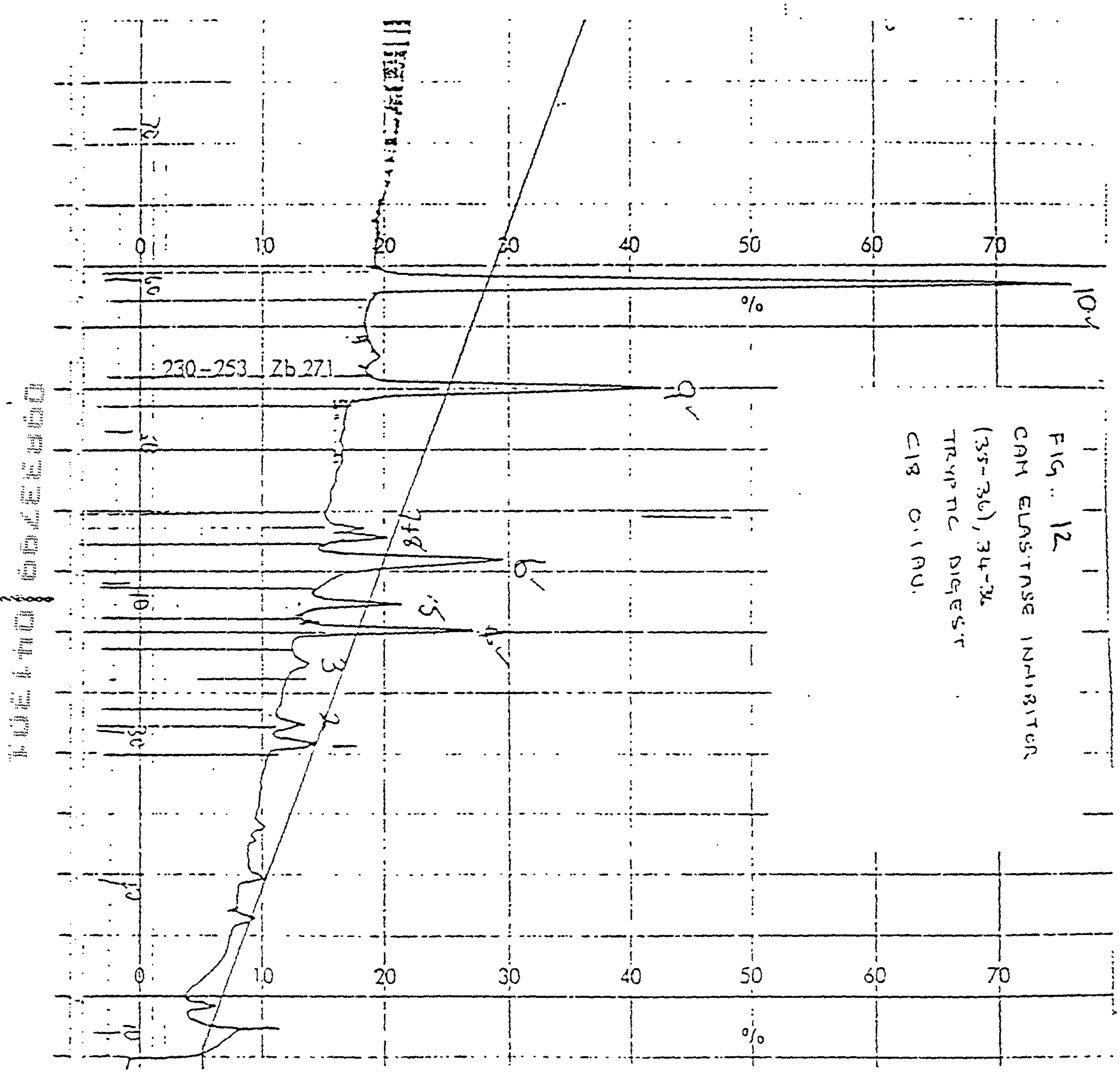


FIG. 12
CAM ELASTASE INHIBITOR
TRYPTIC DIGEST
C18 0.1AU.
230-253 Zb 271
%
0
10
20
30
40
50
60
70

FIG 12

Figure 13

AlaGlnGluProValLysGlyProValSerThr

1 ELI1

AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACT

GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGA

LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg

63 ELI3

AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT

TTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCA

ELI2

CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet

123 ELI5

TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG

ACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATAC

ELI4

AlaCysPheValProGlnEndEnd

183 GCTTGTTTCGTTCCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210

ELI6

Figure 14

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys

GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5′ DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys

CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

Figure 15

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC
5′ DNA
Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln
TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCACACTGTCCA
TTCTTCCTCCCATTCAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACTTTCCAATAAAGAGTTCCG
GAATTC

Poly A signal 3′

Z = T, C or A
P = A or G

FIGURE 16

```
                10                  30                  50
.         .         .         .         .         .
GGAATTCCGGTTCCTCATCGCTGGGACGCTGGTTCTAGAGGCAGCTGTCACGGGAGTTCC
EcoRI                            XbaI
F  L  I  A  G  T  L  V  L  E  A  A  V  T  G  V  P
|--------IN-FRAME UPSTREAM PROTEIN SEQUENCE------
70                  90                  110
.         .         .         .         .         .
TGTTAAAGGTCAAGACACTGTCAAAGGCCGTGTTCCATTCAATGGACAAGATCCCGTTAA
V  K  G  Q  D  T  V  K  G  R  V  P  F  N  G  Q  D  P  V  K
130                 150                 170
.         .         .         .         .         .
AGGACAAGTTTCAGTTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCC
G  Q  V  S  V  K  G  Q  D  K  V  K
AlaGlnGluProValLysGlyPr
|--ELASTASE INHIBITOR--
```

Cont'd 16b of 19

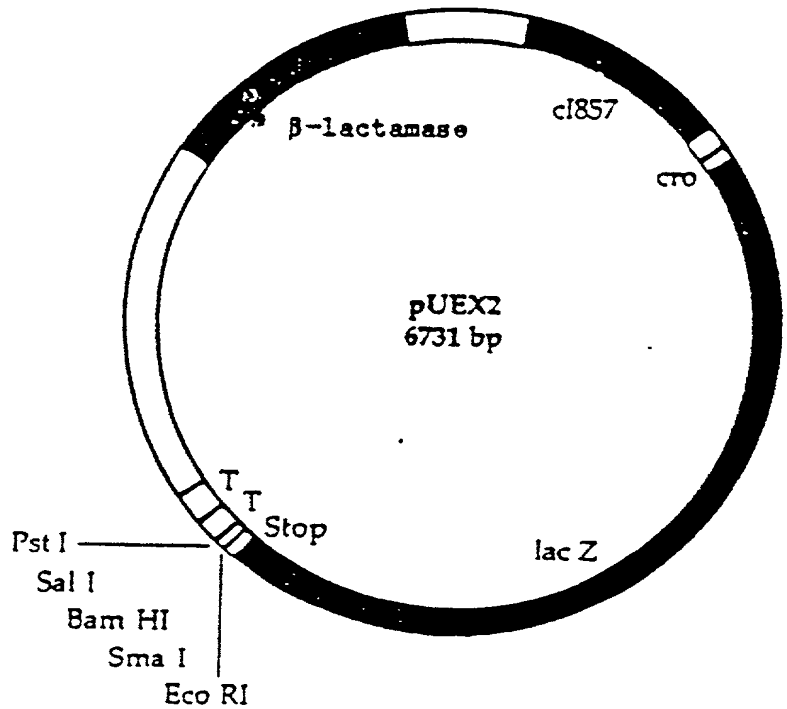
FIGURE 16 CONTINUED

```
     190                 210                 230
      .         .         .         .         .         .
AGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTGATCCGGTGCGCCATGTTGAATCC
oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

     250                 270                 290
      .         .         .         .         .         .
CCCTAACCGCTGCTTGAAAGATACTGACTGCCCAGGAATCAAGAAGTGCTGTGAAGGCTC
oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe
     310                 330                 350
      .         .         .         .         .         .
TTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAGGGAGCCGGTCCTTGCTGCACCTGTGC
rCysGlyMetAlaCysPheValProGlnEnd
     370                 390                 410
      .         .         .         .         .         .
CGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCAC

     430                 450                 470
      .         .         .         .         .         .
ACTGTCCATTCTTCCTCCCATTCAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACT

     490
      .         .
TTCCAATAAAGAGTTCCGGAATTC
       Poly A      EcoRI
       signal
```




```
        EcoRI  SmaI BamHI   SalI          PstI
        |        |    |      |              |
pUEX2   GAA TTC CCG GGG ATC CGT CGA CCT GCA GCC AAG CTT GCT GAT TGA
        Glu Phe Pro Gly Ile Arg Arg Pro Ala Ala Lys Leu Ala Asp ***
```

FIG 17

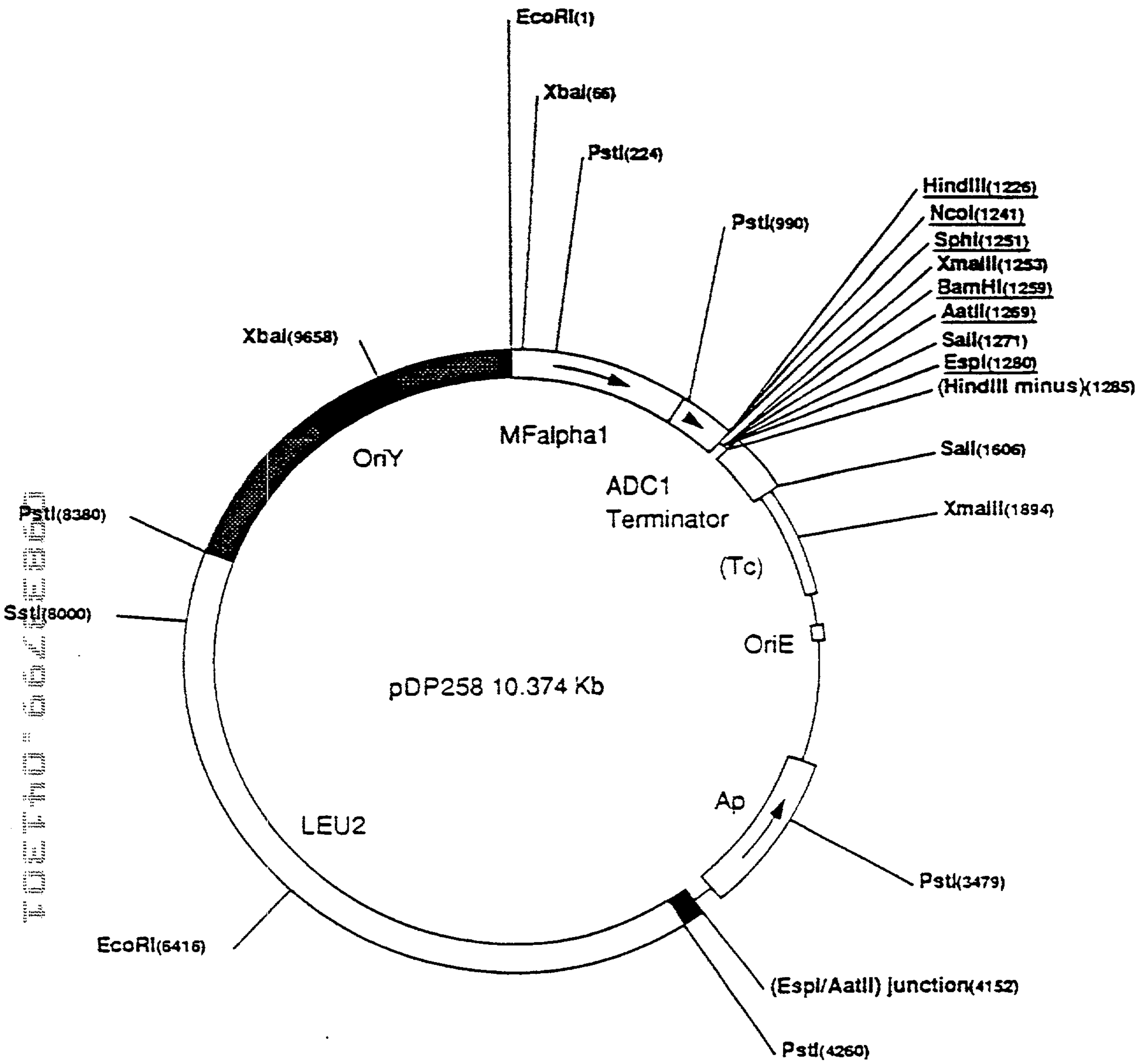
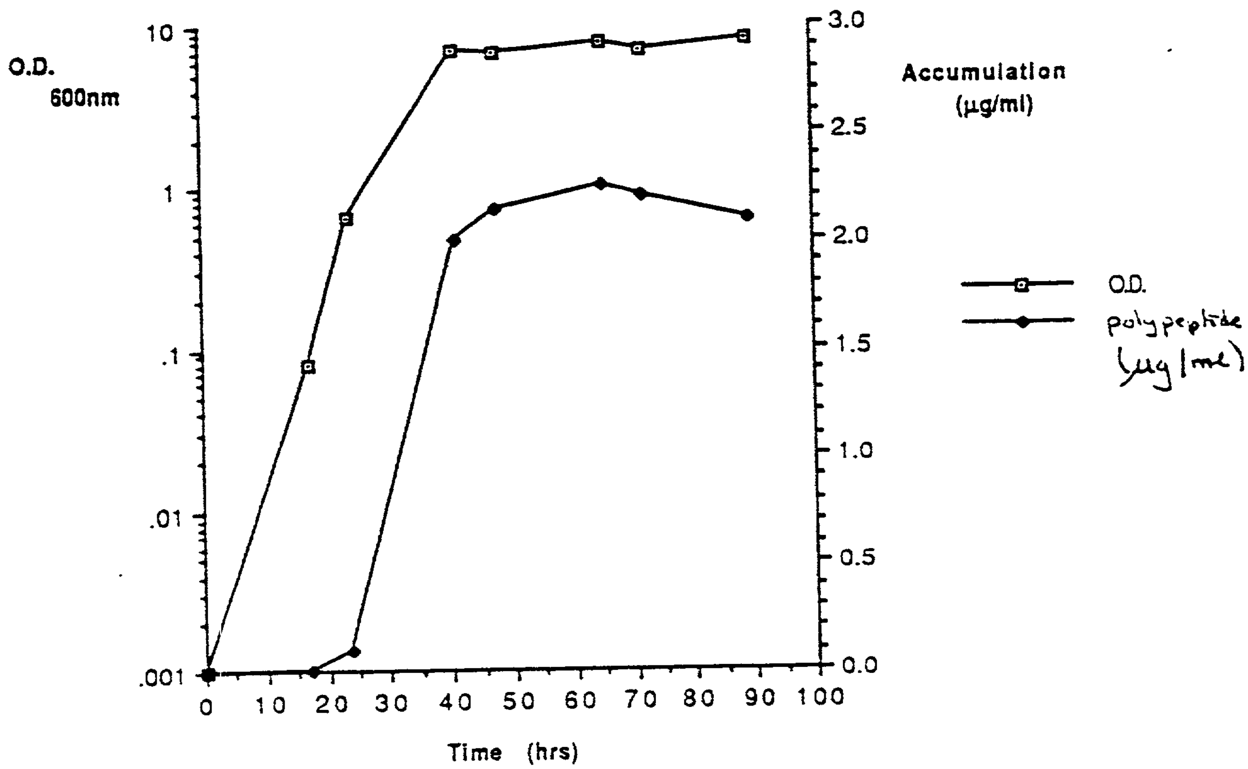

EcoRI(1)
XbaI(66)
PstI(224)
PstI(990)
HindIII(1226)
NcoI(1241)
SphI(1251)
XmaIII(1253)
BamHI(1259)
AatII(1269)
SalI(1271)
EspI(1280)
(HindIII minus)(1285)
SalI(1606)
XmaIII(1894)
PstI(3479)
(EspI/AatII) junction(4152)
PstI(4260)
EcoRI(6416)
SstI(8000)
PstI(8380)
XbaI(9658)
MFalpha1
OriY
ADC1
Terminator
(Tc)
OriE
pDP258 10.374 Kb
Ap
LEU2

FIG 18



O.D.
600nm
10
1
.1
.01
.001
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Accumulation
(µg/ml)
0 10 20 30 40 50 60 70 80 90 100
Time (hrs)
O.D.
polypeptide
(µg/ml)

FIG 19